

Figure S1 Viral titers in wastewater samples processed in chronological groups with Method I. 108 sewage samples (January 8 to May 5) were collected from northern and southern catchments. Top: Viral titers in the wastewater (blue line along the primary y-axis), daily (orange line) and cumulative (light orange) confirmed cases in MA along the secondary y-axis. Viral titers are calculated and averaged from qPCR results with N1 and N2 primers (normalized with PMMoV reference). Shaded area represents the minimum and maximum values. The earliest dates of SARS-CoV-2 detection in sewage samples were March 8 for Northern influent and March 10 for Southern influent. Bottom: Viral titers in northern and southern influents. Grey vertical line: first day of stay-at-home order.

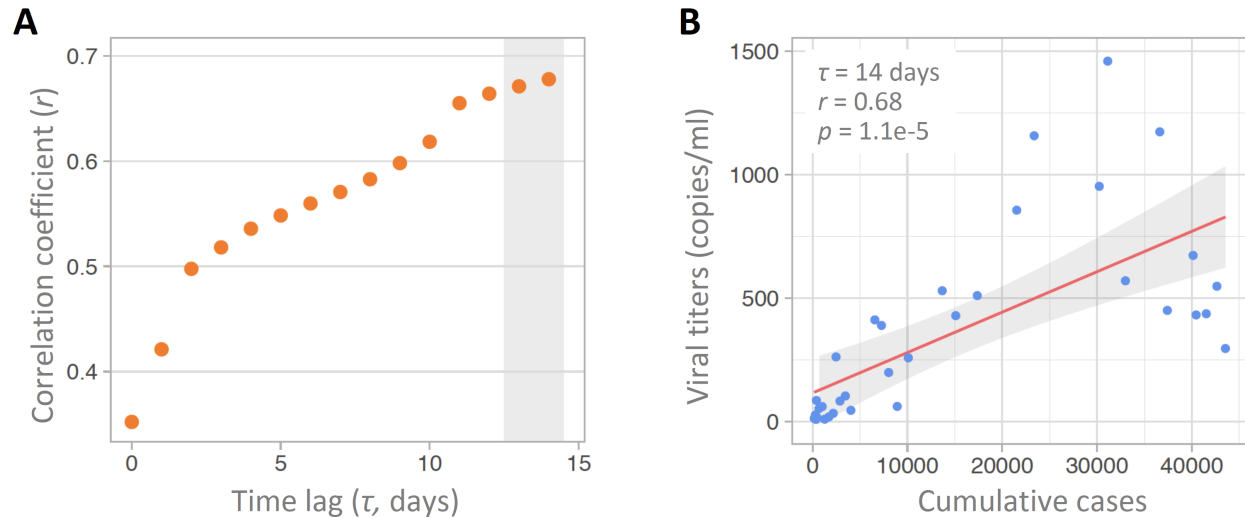


Figure S2 Correlation analysis between viral titers in wastewater and clinically reported cumulative cases, with or without a time lag. (A-B) Linear correlation between unsmoothed viral titers in the northern and southern influents and the number of cumulative cases with different time lags from 0 to 14 days. (B) Viral titers correlate with cumulative cases with a 14 day time lag. Red solid line is the linear regression fitting. Grey area: 95% confidence interval from standard error of the fitting. Pearson's $r = 0.68$, $p = 1.1e-5$.

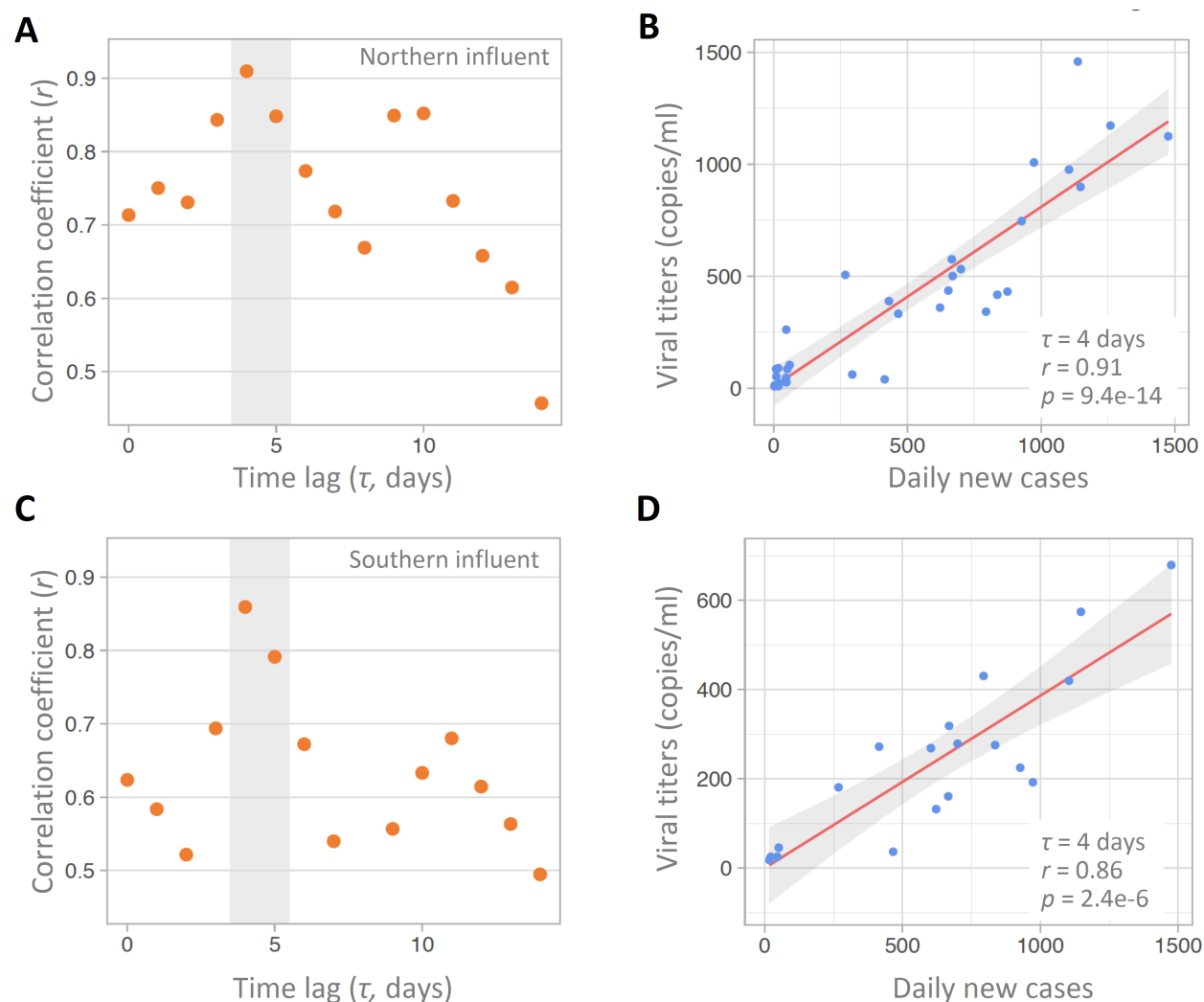


Figure S3 Correlation analysis between viral titers in northern or southern influents and daily new cases, with or without a time lag. (A-B) Linear correlation between unsmoothed viral titers in northern influent and unsmoothed daily new cases with different time lags from 0 to 14 days. Pearson correlation coefficient is highest with a 4 day time lag, with Pearson's $r = 0.91$ and $p = 9.4e-14$. (C-D) Linear correlation between unsmoothed viral titers in southern influent and unsmoothed daily new cases with different time lags from 0 to 14 days. Pearson correlation coefficient is highest with a 4 day time lag, with Pearson's $r = 0.86$ and $p = 2.4e-6$. Red solid line is the linear regression fitting. Grey area: 95% confidence interval from standard error of the fitting.

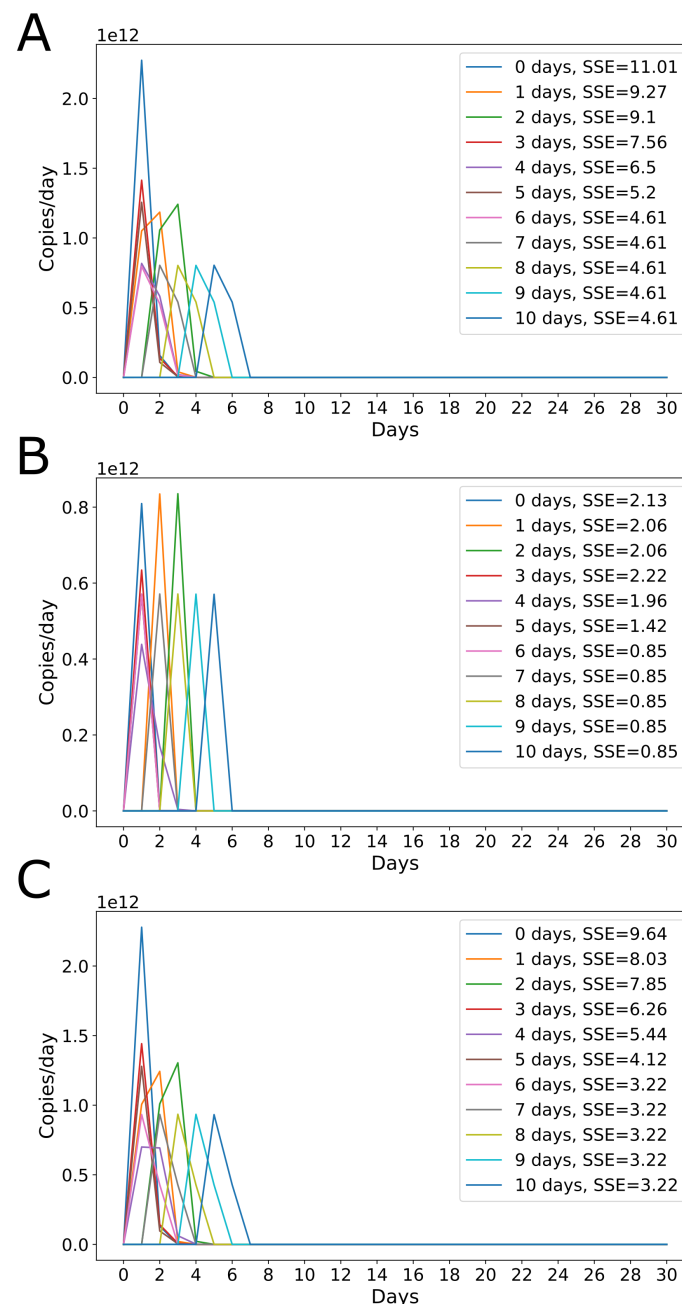


Figure S4 Optimal viral shedding function for various time lags. Allowing clinical time lag to vary between 0-10 days reveals optimal shedding functions for (A) northern influent, (B) southern influent, (C) average of southern and northern influent data sets. The optimal shedding function is sharply peaked for all time lags. The optimal shedding function was multiplied by average wastewater volume of $1.36 \times 10^6 \text{ m}^3$ ($1.36 \times 10^{12} \text{ mL}$) to convert to copies shed per day.

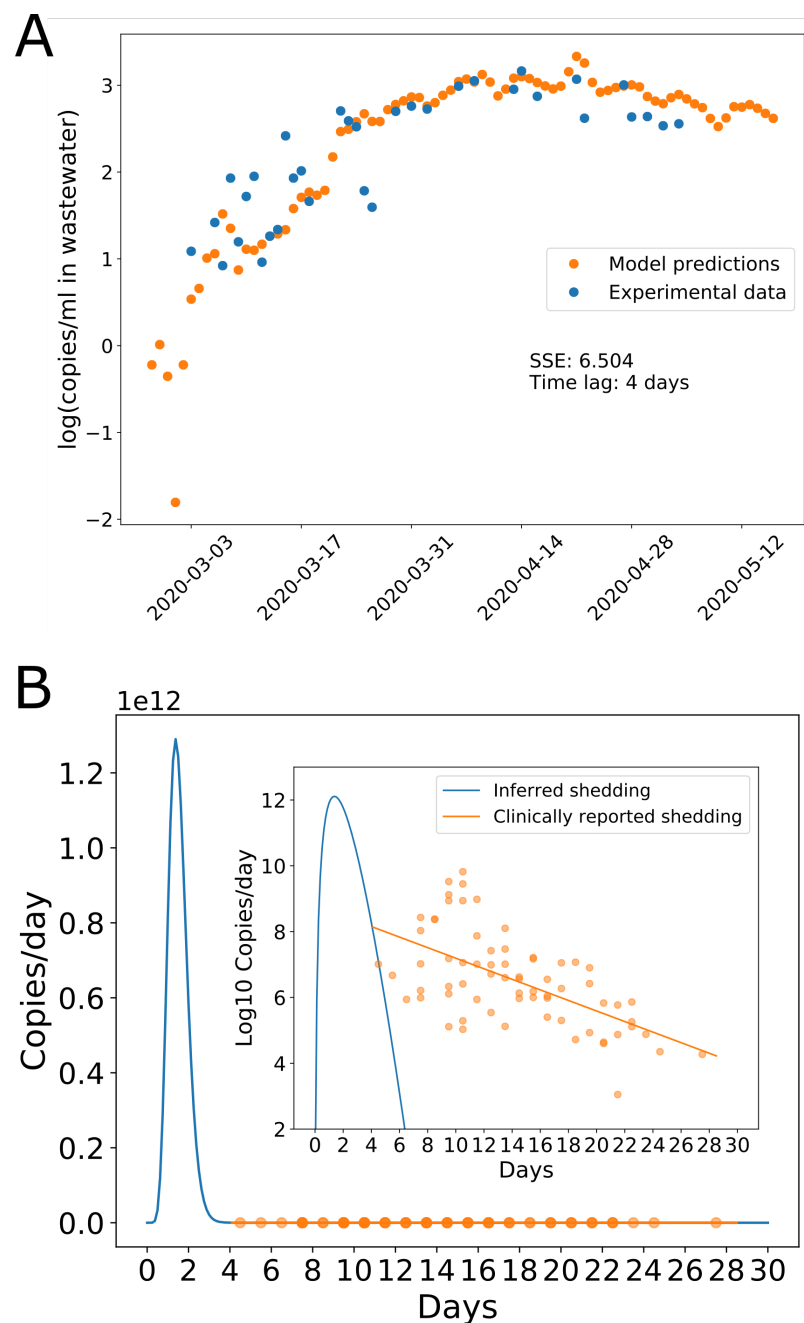


Figure S5 Model fit and optimal shedding function for northern influenza alone, with 4 day time lag. (A) The optimal shedding function minimizes the sum of squared errors between wastewater data (log10) and the convolution of new cases per day $I(t)$ with the individual shedding function $s(t)$ (B). Clinically reported shedding data are shown in (B) for reference, with linear regression fit (18). Inset shows shedding on a log scale.

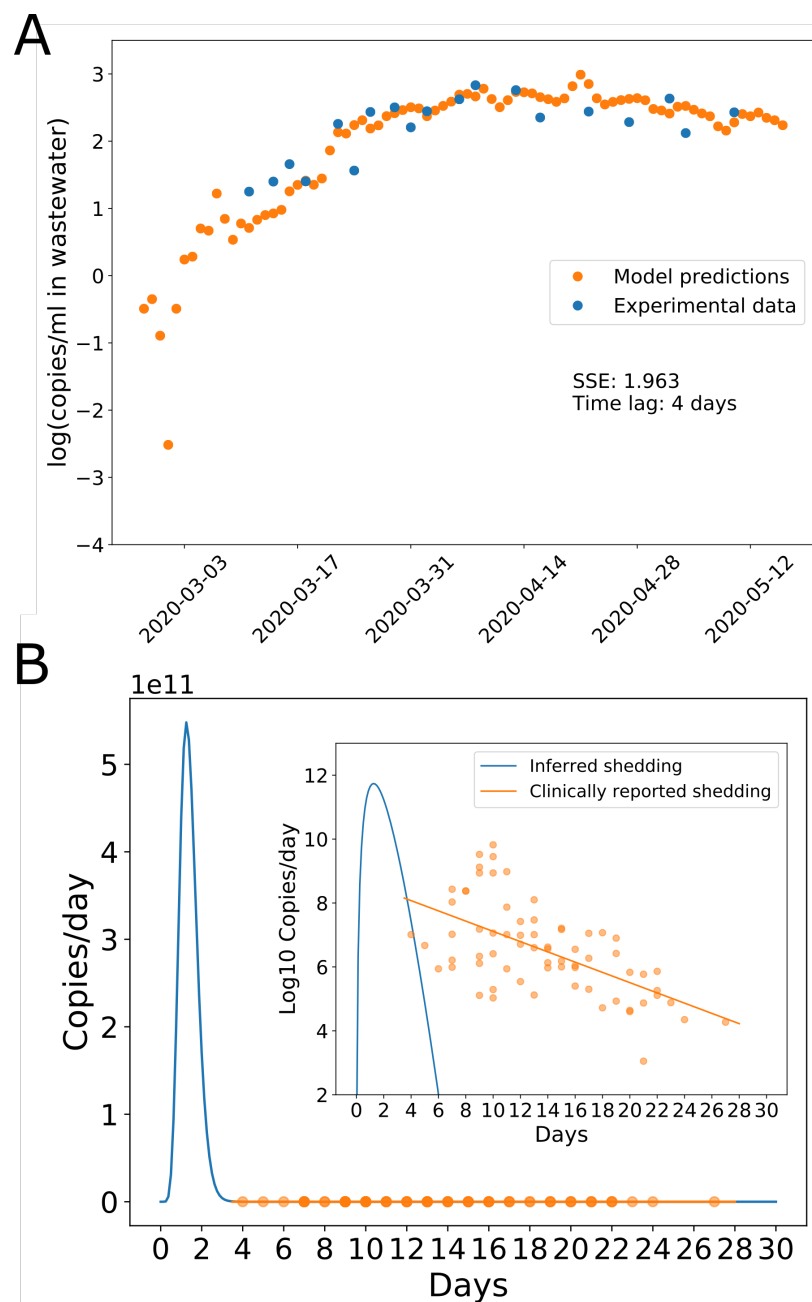


Figure S6 Model fit and optimal shedding function for southern influenza alone, with 4 day time lag. (A) The optimal shedding function minimizes the sum of squared errors between wastewater data (log10) and the convolution of new cases per day $I(t)$ with the individual shedding function $s(t)$ (B). Clinically reported shedding data are shown in (B) for reference, with linear regression fit (18). Inset shows shedding on a log scale.

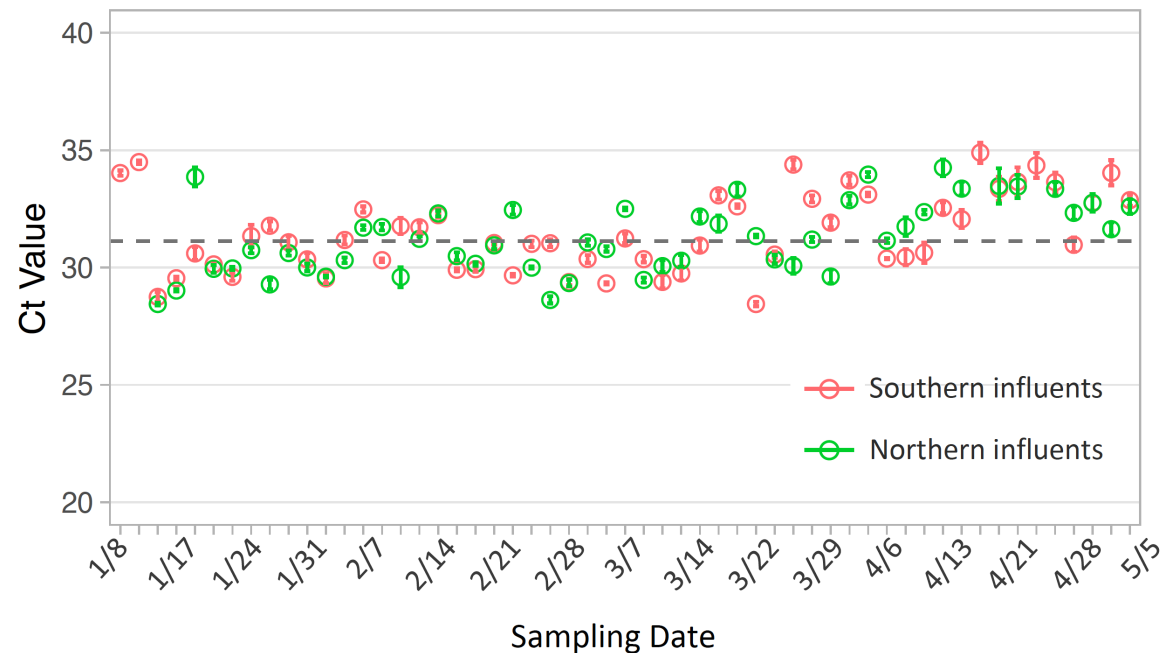


Figure S7 PMMoV Ct values in all the sewage samples collected from January to early May. PMMoV in northern and southern influents varies little over time with the exception of late March. Grey dashed line: median of the Ct value in all the samples. Each data point is the mean \pm sd (standard deviation) from three replicates.

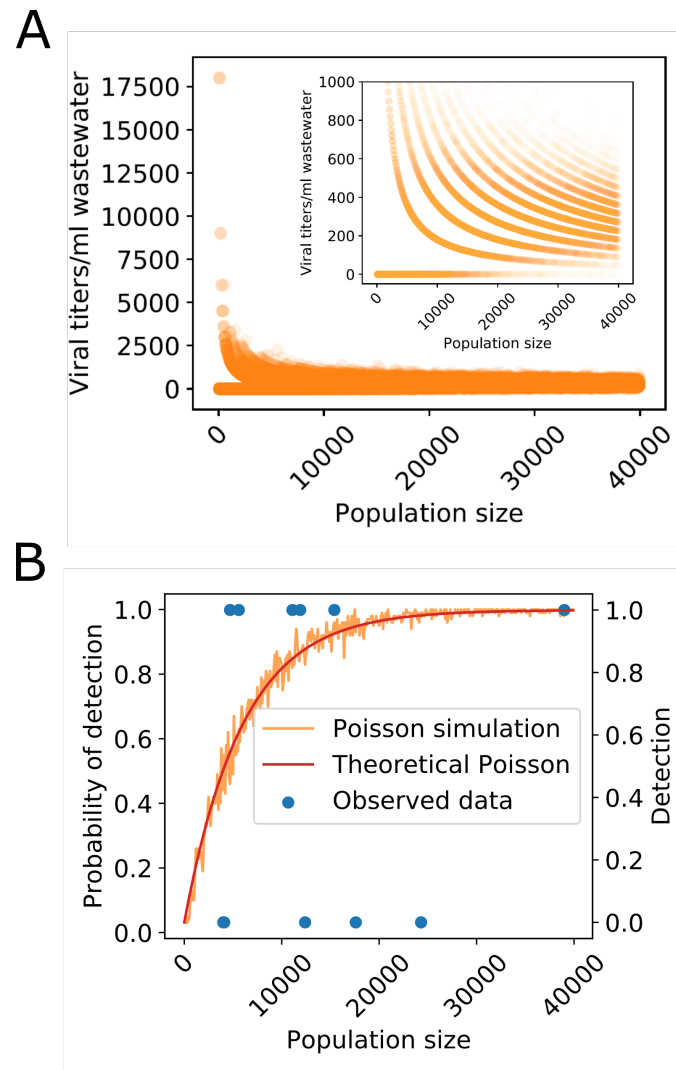


Figure S8 Observed SARS-CoV-2 detection at Massachusetts catchments strongly deviates from a Poisson model that assumes equal incidence across all neighborhoods. (A) Simulating viral titers in different sized catchments using an incidence of 0.00017 (new cases in city during week of sampling / city population / 7 days) and the peak shedding inferred in Figure 1E. Simulated viral titers have high variance at low population sizes, with many non-detects and a few extreme titers. Viral titers converge to the average as population size increases. Inset: zoom in on 0-500 copies/ml wastewater. (B) Observed SARS-CoV-2 detection compared to a theoretical Poisson model with uniform incidence = 0.00017 and the Poisson simulation in (A). Catchments with populations > 15000 should have 100% detection based on the Poisson null model, but observed wastewater detection is 0 for some of those catchments.

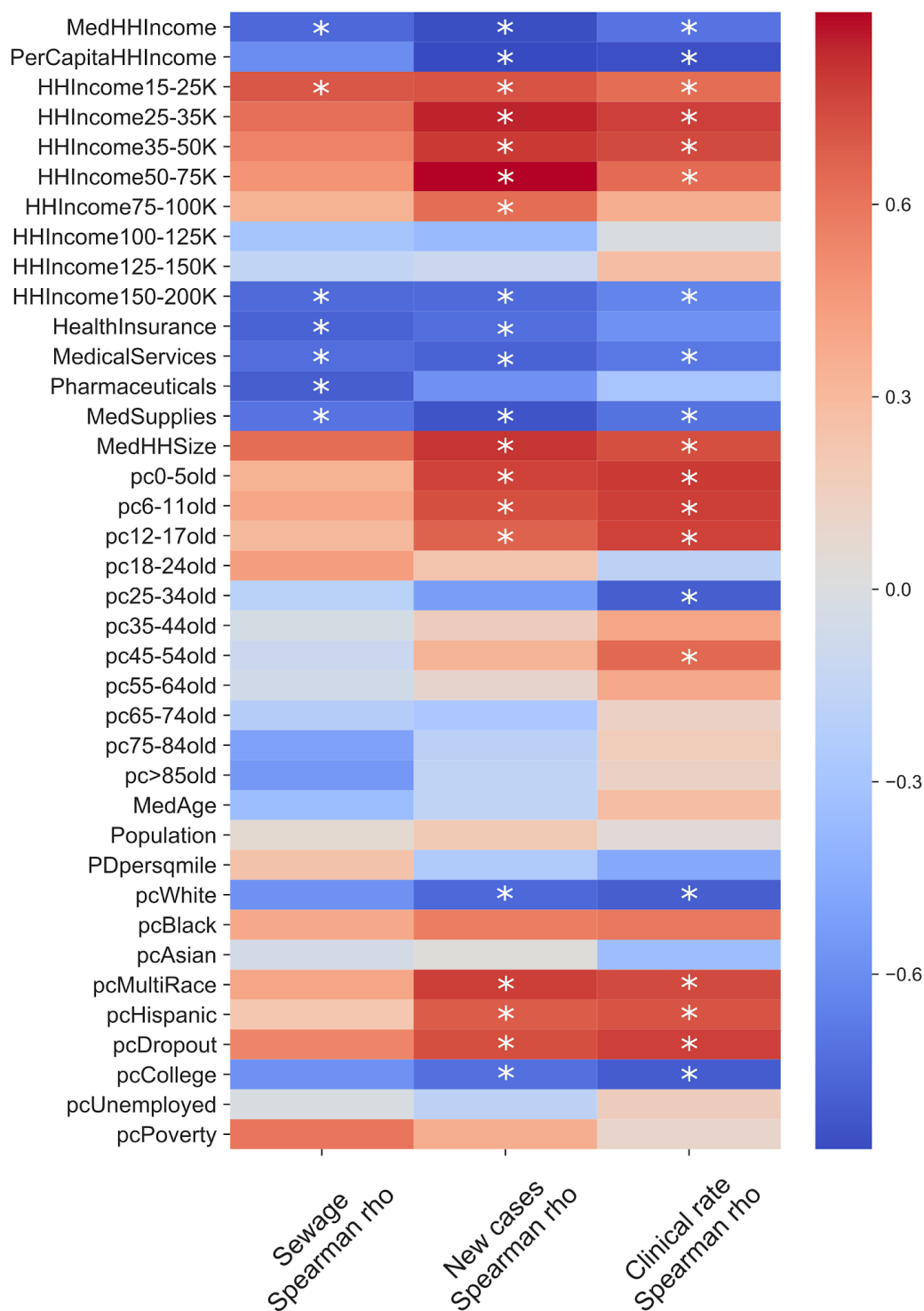


Figure S9 Spearman correlations between sewage titers/clinical data and demographic variables in 11 Boston catchments reveal stronger correlations with demographic variables than with population size. Asterisk denotes significant p-value

at $FDR < 0.1$. pc: percent, HH: household, Ave: average, Med: median. MedHHIncome, PerCapitaHHIncome: Median and Per capita household income. HHIncome15-25K: percentage of population with household income within the range 15-25K throughout the year. HealthInsurance, MedicalServices, Pharmaceuticals, MedSupplies: average household expenditure on health insurance, medical services, pharmaceuticals, and medical supplies. MedHHSIZE: Median household size. pc0-5old: percentage of individuals aged 0-5 years. MedAge: Median age. Population: catchment population size. PDpersqmile: population density per square mile. pcWhite: percentage of individuals identifying as white. pcDropout: percentage of individuals who dropped out of high school. pcCollege: percentage of individuals who completed college. pcUnemployed: percentage of people who are unemployed. pcPoverty: percentage of population in poverty.

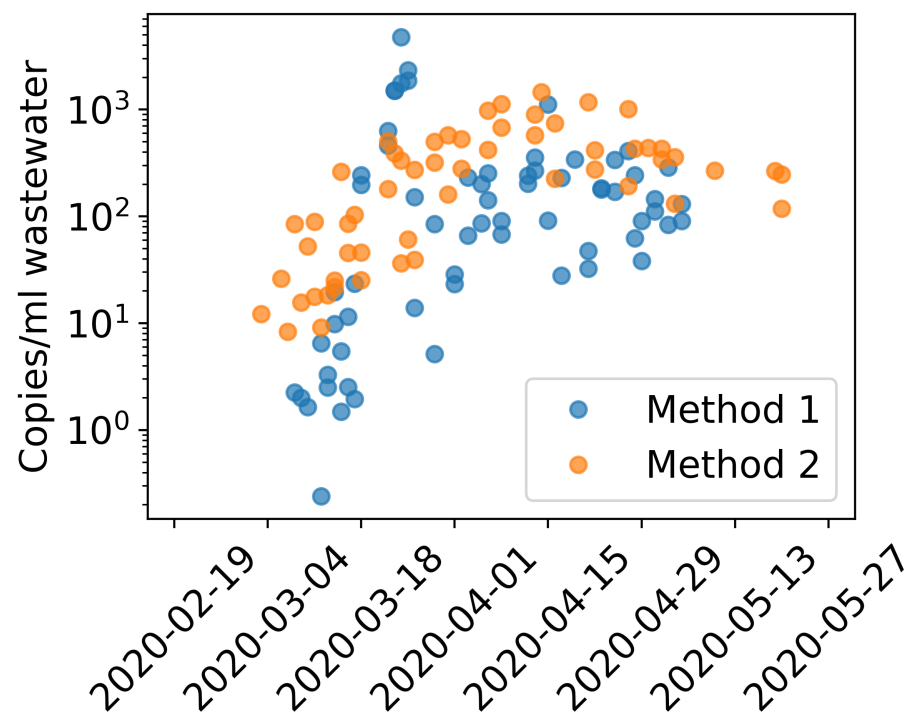


Figure S10 Average normalized viral titers for northern and southern influents using Method 1 vs Method 2 of viral particle precipitation, RNA extraction, and RT-qPCR. Method 1 has a sharp peak and drop off for samples processed in the 3/18-3/25 batch, whereas Method 2 has a smooth increase and plateau.

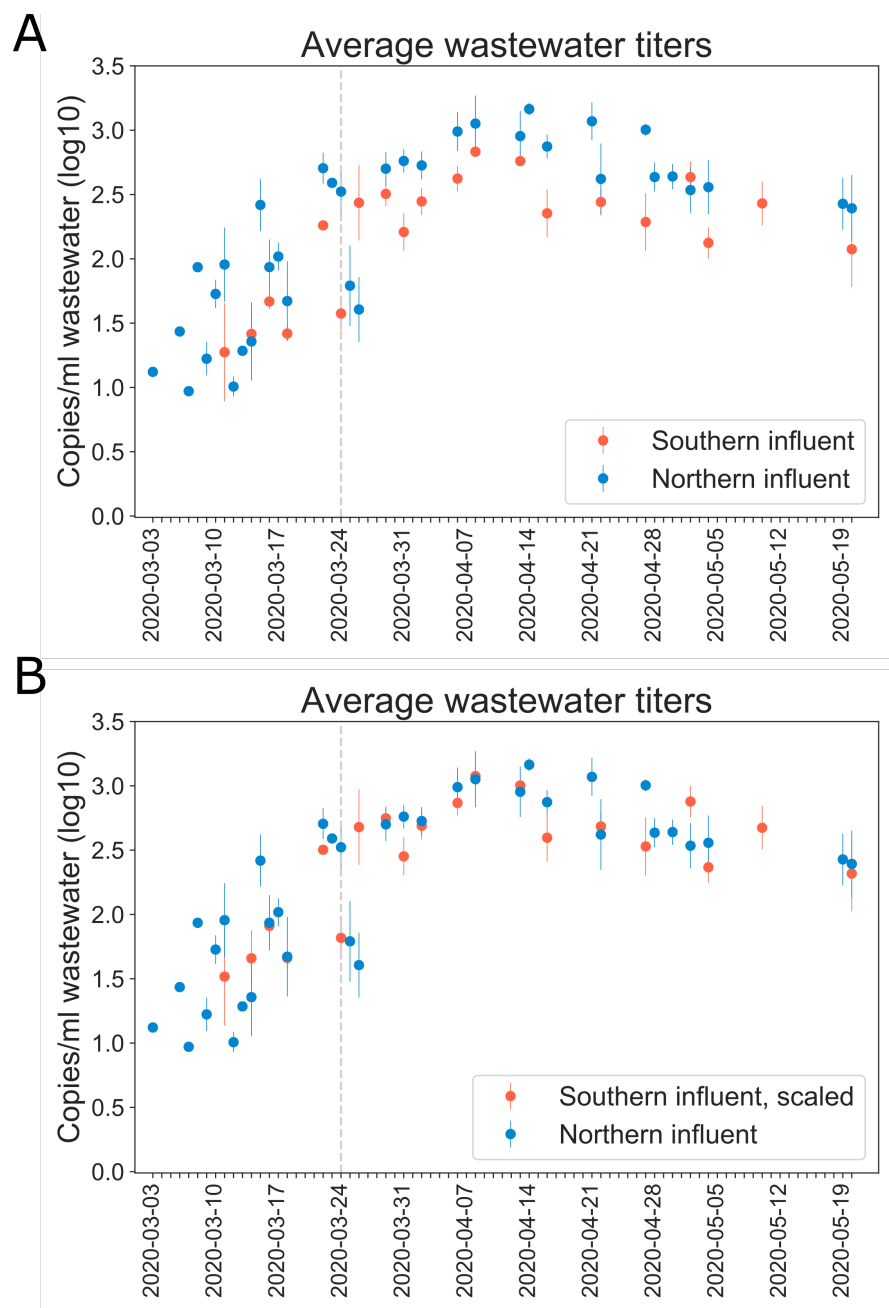


Figure S11 Viral titers in wastewater samples processed with Method II. Samples in northern and southern influents were each processed in one batch. (A) The trends of viral titers in northern and southern influents agreed well, however, absolute value of viral titers differed by a factor of 1.7 that was not observed in Method I. (B) Scaled southern influent data is plotted to match northern data magnitudes. The scaling factor k was found by minimizing the sum of squared errors between southern data $\times k$ and northern data. Grey vertical line: first day of stay-at-home order in Massachusetts.